

Sequence Listing.txt
SEQUENCE LISTING

<110> LUKYANOV, SERGEY A
SHAGIN, DMITRY A
YANUSHEVICH, YURY G

<120> FLUORESCENT PROTEINS AND CHROMOPROTEINS FROM NON-AEQUOREA
HYDROZOA SPECIES AND METHODS FOR USING SAME

<130> U 015745-9
<140> 10/532,681
<141> 2005-04-26

<160> 23

<170> PatentIn version 3.4

<210> 1
<211> 784
<212> DNA
<213> Phialidium sp.

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ggttatggag atgcaagtgt tgtaaagtt gatgcccatt tcatctgcac aactggagat 180
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ttat 784

<210> 2
<211> 234
<212> PRT
<213> Phialidium sp.

<400> 2

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Sequence Listing.txt

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95

Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Glu Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Pro
180 185 190

Val His Val Pro Glu Tyr His His Ile Thr Tyr His Val Thr Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

<210> 3
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<212> DNA
<213> Artificial sequence

<220>
<223> phiYFP-Y1 mutant of the phiYFP

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<210> 4
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<213> Artificial sequence

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<223> phiYFP-Y1 mutant of the phiYFP

<400> 4

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Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
 35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95

Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe
 100 105 110

Sequence Listing.txt

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
180 185 190

Val His Val Pro Glu Tyr His His Met Thr Tyr His Val Thr Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

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<223> phiYFP-M0 mutant of the phiYFP

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cacacccaaa tgaacacacc cattgggtt ggaccagtcc atgcccgtga aaaccatcat 600

Sequence Listing.txt
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<213> Artificial sequence

<220>
<223> phiYFP-M0 mutant of the phiYFP

<400> 6

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1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Arg His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Pro
180 185 190

Sequence Listing.txt

Val His Val Pro Glu Asn His His Met Ser Tyr His Val Lys Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

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<210> 7
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<212> DNA
<213> Artificial sequence
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<220>
<223> phiYFP-M1 mutant of the phiYFP

<210> 8
<211> 234
<212> PRT
<213> Artificial sequence

<220>
<223> phiYFP-M1 mutant of the phiYFP

<400> 8

Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Sequence Listing.txt

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
180 185 190

Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

<210> 9
<211> 705
<212> DNA
<213> Artificial sequence

<220>
<223> humanized version of the phiYFP-M1

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ttctacaaga	gctgcatgcc	cgatggctac	gtgcaggagc	gcaccatcac	cttcgaggcc	300
gatggcaatt	tcaagaccccg	cggcgagggt	accttcgaga	atggcagcgt	gtacaatcgcc	360
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ttcaatttca	ccccccactg	cctgtacatc	tggggcgatc	aggccaatca	cggcctgaag	480
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cacacccaga	tgaataacccc	categgcgcc	ggccccgtgc	acgtgcccga	gtaccaccac	600
atgagctacc	acgtaaagct	gagaaggat	gtgaccgatc	accgcgataa	tatgagcctg	660
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 <213> Artificial sequence

<220>
 <223> humanized version of the phiYFP-M1

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Glu	Met	Glu	Gly	Asn	Val	Asp	Gly	His	Thr	Phe	Ser	Ile	Arg	Gly	Lys
	20					25							30		

Gly	Tyr	Gly	Asp	Ala	Ser	Val	Gly	Lys	Val	Asp	Ala	Gln	Phe	Ile	Cys
35						40					45				

Thr	Thr	Gly	Asp	Val	Pro	Val	Pro	Trp	Ser	Thr	Leu	Val	Thr	Thr	Leu
	50				55						60				

Thr	Tyr	Gly	Ala	Gln	Cys	Phe	Ala	Lys	Tyr	Gly	Pro	Glu	Leu	Lys	Asp
65					70				75			80			

Phe	Tyr	Lys	Ser	Cys	Met	Pro	Asp	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile
		85					90					95			

Thr	Phe	Glu	Gly	Asp	Gly	Asn	Phe	Lys	Thr	Arg	Ala	Glu	Val	Thr	Phe
		100						105					110		

Glu	Asn	Gly	Ser	Val	Tyr	Asn	Arg	Val	Lys	Leu	Asn	Gly	Gln	Gly	Phe

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
 130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
 145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
180 185 190

Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Tyr Leu
225 230

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<210> 11
<211> 1047
<212> DNA
<213> Anthomedusae species

<220>
<221> misc_feature
<223> hydromedusa 1 from sub-order Anthomedusae

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ggtgtcaaaa atttaacgttc tagaaattgc agtacggaag aaaaacccgt catacttggt 180
gcaatgacag aaacatttca gaaaaaaatttgc ccatataaagt tagaatttggatggagatgtt 240
gatggccaaa catttaaggt tatttgttag ggcgttgggg atgcaaccac tggtgtaaat 300
gaaggaaaat atgtttgtac agaaggagaa gttcttattt catgggttcc gtcatcacc 360
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aaaagtactt ttcccttctgg atatcatcaa gaaagaaaaa ttacatatga gaatgtatgtt 480
gttttagaaa cagcagctaa aattactatg gaaagtgggtg caatagtgaa tagaataaaat 540
gtgaaaggca caggcttgcgaa taaagatgtt catgtatgcc aaaaaaaatct tgaatctcc 600
cctcttgcgaa caacatatgt tttcccttgcgaa qqqaqaaqgtt ttcgaaatcat ctatqaaac 660
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cttcaacag atccagaaga aaataaaatgat catattatca tcaaagaaac caactgcgca	840
tttgacgctg attttctta agattccga ttgcataa gattgaaaaa ctaataaaag	900
ataggtaaaa aaaatatgtc ttgtatgtt catacagttat tgatataaagc ttcaaagaaa	960
tatatttca aataaacttt ataaaattag gaatcttga atatataaac taaacctttt	1020
atttgttagaa taaaataat taaagac	1047

<210> 12
 <211> 262
 <212> PRT
 <213> Anthomedusae species

 <220>
 <221> misc_feature
 <223> hydromedusa 1 from sub-order Anthomedusae

<400> 12

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Gly Val Lys Asn Leu Arg Ser Arg Asn Cys Ser Thr Glu Glu Lys Pro		
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Val Ile Leu Gly Ala Met Thr Glu Thr Phe Gln Lys Lys Leu Pro Tyr		
35	40	45

Lys Leu Glu Leu Asp Gly Asp Val Asp Gly Gln Thr Phe Lys Val Ile		
50	55	60

Gly Glu Gly Val Gly Asp Ala Thr Thr Gly Val Ile Glu Gly Lys Tyr			
65	70	75	80

Val Cys Thr Glu Gly Glu Val Pro Ile Ser Trp Val Ser Leu Ile Thr		
85	90	95

Ser Leu Ser Tyr Gly Ala Lys Cys Phe Val Arg Tyr Pro Asn Glu Ile		
100	105	110

Asn Asp Phe Phe Lys Ser Thr Phe Pro Ser Gly Tyr His Gln Glu Arg		
115	120	125

Lys Ile Thr Tyr Glu Asn Asp Gly Val Leu Glu Thr Ala Ala Lys Ile		
130	135	140

Thr Met Glu Ser Gly Ala Ile Val Asn Arg Ile Asn Val Lys Gly Thr
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145 150 155 160

Gly Phe Asp Lys Asp Gly His Val Cys Gln Lys Asn Leu Glu Ser Ser
165 170 175Pro Pro Ser Thr Thr Tyr Val Val Pro Glu Gly Glu Gly Ile Arg Ile
180 185 190Ile Tyr Arg Asn Ile Tyr Pro Thr Lys Asp Gly His Tyr Val Val Ala
195 200 205Asp Thr Gln Gln Val Asn Arg Pro Ile Arg Ala Gln Gly Thr Ser Ala
210 215 220Ile Pro Thr Tyr His His Ile Lys Ser Lys Val Asp Leu Ser Thr Asp
225 230 235 240Pro Glu Glu Asn Lys Asp His Ile Ile Ile Lys Glu Thr Asn Cys Ala
245 250 255Phe Asp Ala Asp Phe Ser
260

<210> 13
<211> 1089
<212> DNA
<213> Anthomedusae species

<220>
<221> misc_feature
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cattatttca atccgatatg acattcaaga tcttcatcg tgagtggtg aatgatcaga 180
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ctgtgtgcga aaccgggaaa ctcccaatgtt catggaaacc tatttgcac ctatccat 300
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ctcaccacac ctatgatgtt gacggcacct gtgtcatttc caggataacc gtaattgtg 480
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agacacatgtt gttccctat gggtccatgtt ctgtcagaca attgtgtac atggcttca 600
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Sequence Listing.txt

<210> 14
<211> 232
<212> PRT
<213> Anthomedusae species

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<220>
<221> misc_feature
<222> http://redmine.2.com/redmine/authenticated
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-1000- 14

Met Glu Gly Gly Pro Ala Leu Phe Gln Ser Asp Met Thr Phe Lys Ile
1 5 10 15

Phe Ile Asp Gly Val Val Asn Asp Gln Lys Phe Thr Ile Ile Ala Asp
20 25 30

Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
35 40 45

Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
50 55 60

Gln Tyr Gly Glu Pro Phe Phe Ala Lys Tyr Pro Asn Gly Ile Ser His
65 70 75 80

Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Thr Ile Asp Arg Thr Val
 85 90 95

Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
100 105 110

Asp Gly Thr Cys Val Ile Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
115 120 125

Gln Pro Asp Gly Pro Ile Met Lys Asp Gln Leu Val Asp Ile Leu Pro
 130 135 140

Sequence Listing.txt

Thr Glu Thr His Met Phe Pro His Gly Ser Asn Ala Val Arg Gln Leu
145 150 155 160

Cys Tyr Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His
165 170 175

Phe Asp Ser Lys Leu Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro
180 185 190

Gly Pro His Phe Val Thr Val Ile Ile Lys Gln Met Lys Asp Thr Ser
195 200 205

Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
210 215 220

Val Pro Arg Ile Thr Ser Ala Ile
225 230

<210> 15
<211> 699
<212> DNA
<213> Artificial sequence

<220>
<223> S3-2 mutant of the hm2CP from a hydromedusa 2 from sub-order
Anthomedusae

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gacttcaacg tacatgtgt gtgcgaaacc gggaaactcc caatgtcatg gaaacccatt 180
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acccaaacaga tgaaagatac aagegacaag cgtgtatcatg tggatccagg ggaagtccacc 660
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<210> 16
<211> 232
<212> PRT

Sequence Listing.txt

<213> Artificial sequence

<220>

<223> S3-2 mutant of the hm2CP from a hydromedusa 2 from sub-order
Anthomedusae

<400> 16

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20 25 30Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
35 40 45Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
50 55 60Gln Tyr Gly Glu Pro Phe Ala Arg Tyr Pro Asn Gly Ile Ser His
65 70 75 80Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Ser Ile Asp Arg Thr Val
85 90 95Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
100 105 110Asp Gly Thr Cys Val Val Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
115 120 125Gln Pro Asp Gly Pro Ile Met Arg Asp Gln Leu Val Asp Ile Leu Pro
130 135 140Asn Glu Thr His Met Phe Pro His Gly Pro Asn Ala Val Arg Gln Leu
145 150 155 160Ala Phe Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His
165 170 175Phe Asp Ser Lys Met Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro
180 185 190Gly Pro His Phe Val Thr Thr Ile Thr Lys Gln Met Lys Asp Thr Ser
195 200 205Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
210 215 220

Sequence Listing.txt

Val Pro Arg Ile Thr Ser Ala Ile
225 230

<210> 17
<211> 705
<212> DNA
<213> Artificial sequence

<220>
<223> phiYFP-M1G1 mutant, derived from humanized version of the
phiYFP-M1

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gtgaccaccc tgcctacagg cggccagtgc ttccccaatgc acggcccgaa gctgaaggat 240
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<210> 18
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<212> PRT
<213> Artificial sequence

<220>
<223> phiYFP-M1G1 mutant, derived from humanized version of the
phiYFP-M1

<400> 18

Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Sequence Listing.txt

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
 50 55 60

Ser Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
 65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
 85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
 100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
 115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
 130 135 140

Pro His Cys Gln Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
 145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
 165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
 180 185 190

Val His Val Pro Glu Tyr His His Met Ser Thr His Val Lys Leu Ser
 195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
 210 215 220

Arg Ala Val Asp Cys Arg Thr Ala Tyr Leu
 225 230

<210> 19
 <211> 705
 <212> DNA
 <213> Artificial sequence

<220>
 <223> phiYFP-M1C1 mutant, derived from humanized version of the
 phiYFP-M1

<400> 19
 atgtccagcg gcgcccgact gttccacggc aagatccccct acgtggtgga gatggagggc 60
 aatgtggatg gccacacctt cagcatccgc ggcagaaggct acggcgatgc cagcgtggcc
 aagggtggatg cccagttcat ctgcaccacc ggcgatgtgc ccgtgcccgt gagcacccctg 120
 Page 16 180

Sequence Listing.txt

gtgaccaccc tgcctctgggg cgcccaagtgc ttgcccaagt acggccccga gctgaaggat 240
ttctacaaga gctgcattgcg cgtatggctac gtgcaggagc gcaccatcac cttcgaggc 300
gtatggcaatt tcaagacccg cgccgagggtg accttcgaga atggcagcgt gtacaatcgc 360
gttgaagctga aaggccagggtt cttcaagaag gatggccacg tgctggccaa gaatctggag 420
ttcaatttca ccccccacta ccagatcacatc tggggcgtac aggcataatca cggcctgaag 480
agcgccttca agatctgcac cggatcacc ggcagtaagg gcatgttcat cttggcccgat 540
cacacccaga tgaatacccc catcgccgcg ggccccgtgc acgtgcccga gtaccaccac 600
atgagcaccc acgtgaagct gagaaggat gtgaccgatc accgcgataaa tatgagcctg 660
aaggagaccc tgcgcgcgtt ggattggccgc aagacctacc ttgtga 705

<210> 20
<211> 234
<212> PRT
<213> Artificial sequence

<220>
<223> phiYFP-M1C1 mutant, derived from humanized version of the
phiYFP-M1

<400> 20

Met Ser Ser Gly Ala Gln Leu Phe His Gly Lys Ile Pro Tyr Val Val
1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

Ser Trp Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Lys Gly Gln Gly Phe
115 120 125

Sequence Listing.txt

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
 130 135 140

Pro His Tyr Gln Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
 145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
 165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
 180 185 190

Val His Val Pro Glu Tyr His His Met Ser Thr His Val Lys Leu Ser
 195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Leu
 210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
 225 230

<210> 21
 <211> 699
 <212> DNA
 <213> Artificial sequence

<220>
 <223> humanized version of the S3-2 mutant of hm2CP from a hydromedusa
 2 from sub-order Anthomedusae

<400> 21	
atggaggggcg gccccggcct gttccagagc gacatgacct tcaaaatctt catcgacggc	60
gtggtaacg gccagaagtt caccatgtg gccgacggca gcagcaagtt ccccaacggc	120
gacttcaacg tgacggccgt gtgcgagacc ggcaagctgc ccatgagctg gaagccatc	180
tgccccctga tccagtaegg cgagcccttc ttgcggcgct accccaaacgg catcageccac	240
ttcgcccaagg atgtttccc cgaggccctg agcatcgacc gcacccgtgcg cttcgagaac	300
gacggccatca tgaccagccca ccacacctac gagctggacg gcacccgtgcg ggtgagccgc	360
ataccgtgtca actcgacgg ctccagcccc gacggccccca tcatgcgcga ccagctgggt	420
gacatccgtgc ccaacggacat ccacatgttc ccccaacggcc ccaacgcgt gcgcacgtgc	480
gccttcatcg gcttcaccac cgccgacggc ggctgtatga tgagccactt cgacagcaag	540
atgacccatca acggcagccg cgccatcaag atccccggcc cccacttcgt gaccaccatc	600
accaagcaga tgaaggacac cagcgacaaag cgccgaccacg tgcggccatcg cgaggtgacc	660
tacgccccaca gctgtcccccg catcaccaggc gccatctga	699

Sequence Listing.txt

<210> 22
<211> 232
<212> PRT
<213> Artificial sequence

<220>
<223> humanized S3-2 mutant of hm2CP from a hydromedusa 2 from
sub-order Anthomedusae

<400> 22

Met Glu Gly Gly Pro Ala Leu Phe Gln Ser Asp Met Thr Phe Lys Ile
1 5 10 15

Phe Ile Asp Gly Val Val Asn Gly Gln Lys Phe Thr Ile Val Ala Asp
20 25 30

Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
35 40 45

Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
50 55 60

Gln Tyr Gly Glu Pro Phe Phe Ala Arg Tyr Pro Asn Gly Ile Ser His
65 70 75 80

Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Ser Ile Asp Arg Thr Val
85 90 95

Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
100 105 110

Asp Gly Thr Cys Val Val Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
115 120 125

Gln Pro Asp Gly Pro Ile Met Arg Asp Gln Leu Val Asp Ile Leu Pro
130 135 140

Asn Glu Thr His Met Phe Pro His Gly Pro Asn Ala Val Arg Gln Leu
145 150 155 160

Ala Phe Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His
165 170 175

Phe Asp Ser Lys Met Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro
180 185 190

Gly Pro His Phe Val Thr Thr Ile Thr Lys Gln Met Lys Asp Thr Ser
195 200 205

Sequence Listing.txt

Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
210 215 220

Val Pro Arg Ile Thr Ser Ala Ile
225 230

<210> 23
<211> 238
<212> PRT
<213> Aequorea victoria

<400> 23

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Sequence Listing.txt

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235